

FIGURE 1

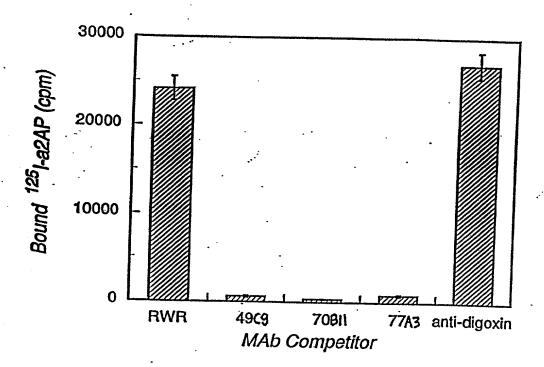


FIGURE 2

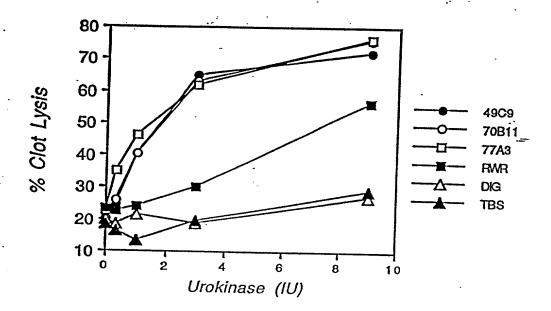


FIGURE 3

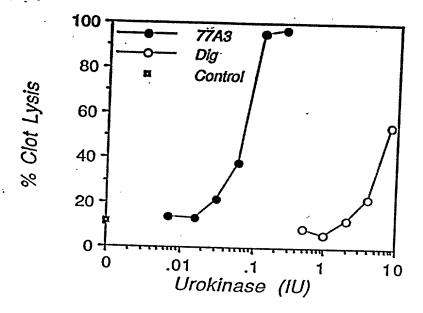
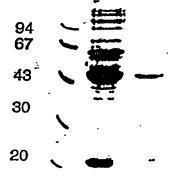


FIGURE 4



Std Ascites 77A3

FIGURE 5

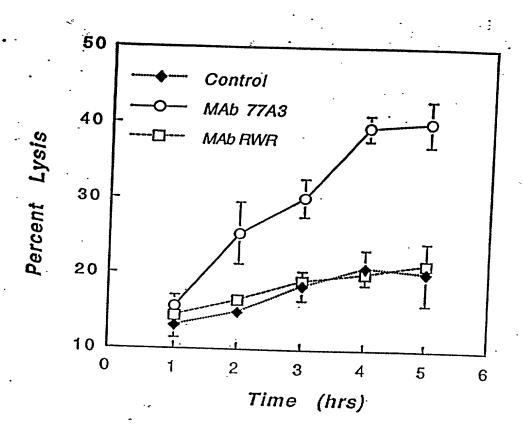


FIGURE 6

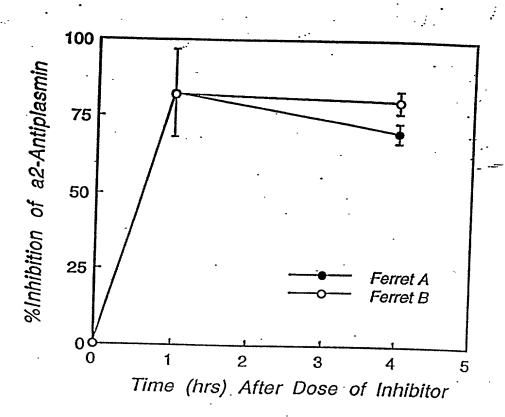


FIGURE 7

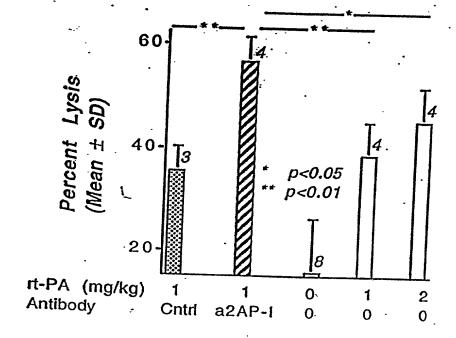


FIGURE 8

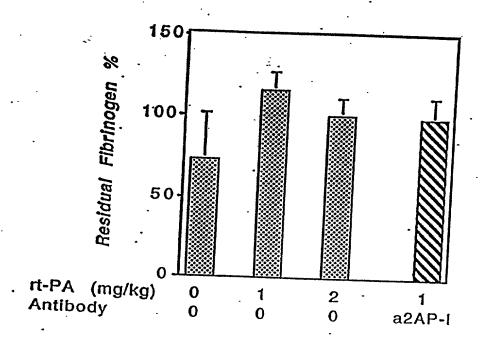


FIGURE 9

Fig. 10

MAb Light Chain

Amino Terminal Sequence

49C9

xIQMTQSPASLSASV

70B11

DIQMT

77A3

xIQMTQSPASLSASV

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Fig. 12

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v	T	C	R	A	s	G	N	I	H	N	Y	L	A	W	Ý	Q	Q	K	Q>
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* *

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ATC	ACA'	TGTC	GA	.GCA	AGT	GG	GAAT	TTA	CAC	AAT	TAT:	TTAG	CA	TGG	TAT	CA	GCAG	AAA	CAG
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H2 HC (49c9 heavy chain) Fig. 14

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	AGA!	249 *	AAG		W 259 *	M	G	W 2	1 69 *	N TTTG	T	K 279 *	s	G	E 289 * CAGCA	P	T GCC	Y 2 CAT	A> 99 *
TGA	AGA!	249 * GTTC	AAG	GGP	W 259 * CGGT	M	g TGTC	W 2 CTTC	1 69 * TC	N TTTG	T GAF	K 279 * ACC	S TC	G TGC	E 289 * CAGCA	P	T GCC	Y 2 CAT	A> 99 * TT
TGA	AGA!	249 * GTTC	AAG	GGP	W 259 * CGGT R	M Tr	v TGT(W 2 CTTC F	1 69 * TC S	n TTTG L	T GAZ E	K 279 * AACC T	TC:	G TGC	E 289 * CAGCA	P CI T	T GCC	Y 2 CAT H	A> 99 * TT
TGA	AGA!	249 * GTTC F	AAG	GGP	W 259 * CGGT R	M Tr	g TGTC	W 2 CTTC F	1 69 * TC S	N TTTG	T GAZ E	K 279 * AACC T	TC:	G TGC	E 289 * CAGCA S	P CI T	T GCC	Y 2 CAT H	A> 99 * TT L>
TGA/ E	AGA E	249 * F F 309	AAG K	GG <i>P</i> G	259 ** *CGGT R 319	M TT	G TGT(V	W 2 CTTC F	1 69 * TC S	n TTTG L	T GAZ E	X 279 ** *ACC T 339 *	TC's	G TGC0 A	E 289 * CAGCA S	P	T GCC A	Y 2 CAT H 3	A> 99 * TT L> 59 *
TGA/ E	AGA E SAT	249 * F F 309	AAG K	GG <i>P</i> G	259 ** *CGGT R 319	M TT	G TGT(V	W 2 CTTC F	1 69 * TC S	TTTG	T GAF E	X 279 ** *ACC T 339 *	TC's	G TGC0 A	E 289 * CAGCA S 349 *	P	T GCC A	Y 2 CAT H 3	A> 99 * TT L> 59 * CC
TGA# E	AGA E SAT	249 * STTC F 309 * CAAG	AAG K AAT	GGP G TTC	W 259 * *CGGT R 319 * *AGAA	M F F	G TGT(V	W 2 CTTC F 3	1 69 *TC S 29 *	TTTG L GGCT	T GAF E	X 279 *AACC T 339 *	TC:	G TGC A CTG	E 289 * CAGCA S 349 * TGCAA	P CT T	T GCC A	Y 2 CAT H 3	A> 99 * TT L> 59 *
TGA# E	AGA E SAT	249 * TTC F 309 *	AAG K AAT	GGP G TTC	W 259 ** *CGGT R 319 **	M F F	G V TGAG E	W 2 CTTC F 3	1 69 * TC S 29 * AC T	TTTG L GGCT	T GAF E	X 279 *ACC T 339 *	TC:	G TGC A CTG	E 289 * CAGCA S 349 * TGCAA	P CT T	T GCC A	Y 2 CAT H 3	A> 99 * TT L> 59 *
TGAA E GCAG Q	AGA E SAT	249 * STTC F 309 * CAAG K 369	AAG K AAT N	GGF G TTC F	W 259 ** *CGGT R 319 ** *AGAA R 379 *	M TT F	G V V TGAG E	W 2 CTTC F 3 GGAC D	1	TTTG L GGCT	T E E ACF	X 279 * ACC T 339 * * * * * * * * * * * * * * * * * *	TC'S	G TGC: A CTG: C	E 289 ** CAGCA S 349 ** IGCAA A 409 **	P CT T	T A TGG W	2 CAT H 3 GTA V	A> 99 * TT L> 59 *
TGAA E GCAG Q	AGA E GAT I	249 * STTC F 309 * CAAG K 369	AAG K AAT N	GGF G TTC F	W 259 ** *CGGT R 319 ** *AGAA R 379 *	M TT F	G V V TGAG E	W 2 CTTC F 3 GGAC D 3 GGGT	1	TTTG L GGCT	T E E ACF	X 279 * ACC T 339 * * * * * * * * * * * * * * * * * *	TC'S	G TGC: A CTG: C	E 289 * CAGCA S 349 * TGCAA A 409	P CT T	T A TGG W	2 CAT H 3 GTA V	A> 99 * TT L> 59 *

H4 HC (77A3 heavy chain) Fig. 16

		10				20			30			40				50			60
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		*				*			*			*				*			*
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I	Q	L	V	Q	S	G	P	E	L	K	K	₽	G	E	T	V	K	I	S>
		130			1	40			150			160 *			1	.70			180
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g gaa	K GAG	G 250 * TTCA	L AG	K GGA	W 2 CGG	M 60 * TT	G TGCC	W	1 270 * TCT	n TTG	T GAA	K 280 * ACCT	S	G GCC	E 2	90 * AC	T TGCC	Y	A> 300 *
g gaa	K GAG	G 250 * TTCA	L AG	K GGA	W 2 CGG R	M 60 * TT	G TGCC	W TTC F	1 270 * TCT	n TTG	T GAA	K 280 * ACCT	S	G GCC	E 2 AGC S	90 * AC	T TGCC	Y TAA: N	A> 300 * TTG
g gaa	K GAG	G 250 * TTCA F	L AG	K GGA	W 2 CGG R	M 60 * TT F	G TGCC	W TTC F	1 270 * TCT S	n TTG	T GAA	K 280 * ACCT T	S	G GCC	E 2 AGC S	90 * AC T	T TGCC	Y TAA: N	A> 300 * TTG L>
G GAA E	K GAG E	G 250 * TTCA F 310	AG K	K GGA G	W 2 CGG R 3	M 60 TT F 20	G TGCC A	W TTC F	270 * ETCT S 330	n TTG L	T GAA E	X 280 * ACCT T 340 *	S CT S	G GCC A	E 2 AGC S 3	P :90 * AC T :50	TGCC A	Y AAT N	A> 300 * TTG L> 360 *
G GAA E	K GAG E ATC	G 250 * TTCA F 310	AG K	K GGA G	W 2 CGG R 3	M 60 TT F 20	G TGCC A	W TTC F	270 * ETCT S 330 *	n TTG L	T GAA E	X 280 * ACCT T 340 *	S CT S	G GCC A	E 2 AGC S 3	P :90 * AC T :50	TGCC A	Y AAT N	A> 300 * TTG L> 360 *
G GAA E CAG	K GAG E ATC	G 250 * TTCA F 310 * AAGA K	AG K	K GGA G CTC	W 2 CGG R 3 AAA K	M 60 TT F 20 * AA N	TGCC A	TTC F	I 270 * TCT S 330 * EACG	N TTG L	T GAA E ACA	K 280 * ACCT T 340 * TATT	SCTS	G GCC A TGT	E 2 AGC S 3 GCA A	90 *AC T *50 *AG R	TGCC A	Y AAT N	A> 300 * TTG L> 360 *
G GAA E CAG	K GAG E ATC	G 250 * TTCA F 310 * AAGA K 370	AG K	K GGA G CTC	W 2 CGG R 3 AAA K	M 60 * TT F 20 * AA N 80	TGCC A	TTC F	270 * 27CT S 330 * EACG T	N TTG L	T GAA E ACA	X 280 * ACCT T 340 * TATT Y	SCTS	G GCC A TGT	E 2 AGC S 3 GCA A	90 *AC T :50 *AG R	TGCC A	Y AAT N	A> 300 * TTG L> 360 *
G GAA E CAG	K GAG E ATC I	G 250 * TTCA F 310 * AAGA K 370 *	AG K	K G G CTC L	W 2 CGG R 3 AAA K	M 60 * TT F 20 * AA N 80 *	G TGCC A TGAG E	W F GAC	270 * 27CT S 330 * 2ACG T 390	TTG L GCT A	T GAA E ACA T	X 280 * ACCT T 340 * TATT Y 400 *	S CT S TC F	G A TGT C	E 2 2 3 3 GCA A	P * 90 * AC T * AG R * 10 *	TGCC A ATGG	Y AAT N GTA	A> 300 * TTG L> 360 *
G GAA E CAG	GAG E ATC I	G 250 * TTCA F 310 * AAGA K 370	AG K	K G G CTC L	W 2 CGG R 3 AAA K	M 60 * TT F 20 * AA N 80 *	G TGCC A TGAG E	W F GAC	270 * 27CT S 330 * 2ACG T 390	TTG L GCT A	T GAA E ACA T	X 280 * ACCT T 340 * TATT Y 400 *	S CT S TC F	G A TGT C	E 2 2 3 3 GCA A	P * 90 * AC T * AG R * 10 *	TGCC A ATGG	Y AAT N GTA	A> 300 * TTG L> 360 *

Figure 1

A THE WA 13 \$ K 40 THE TEN ENE AND TEN OTE ENG ONE EOC ANE ONE ONE ONE NEE ONA TOT EEN EOG TET NE مدن مدن درد مدت دمن ورد جدن ددن مدن عين جين جين جين جين يعن جيب مذه عين عجد معم ع æ W T F G G G T K L E I red dog me core core ace and ere dan are acc core and core core are and can and ď Ġ E h 77A3-1 and h 77A3 -2 LIGHT CHAIN T1 Loop Signal Peptide L A L3 Loop CΩ 1 S S L Q P B D F G S H Y C Q H F W T T P AND NO LOCATED FOR AND ACCOUNT OF THE WAY TO P P AND SECULO SECUEDO SECULO SECU × L2 Loop ATT TAA ATT GAT ATC TCC TIA GGT CTC GAG h TTA3V L h77A3VL Humanized (aa) NTTA3VL. Humanized (aa) Humanized m (sense) Humanized (aa) Humanized m (sense) Humanized m (anti-sense) Humanized (aa) Humanized nt (sense) Humanized nt (anti-sense) Humanized nt (anti-sense)

h 77/43-1 HEAVY CHAIN SEQUENCES

Signal Peptide

Humanized (aa) Humanized nt (sense) Humanized nt (anti-sense)	h77A3-1	MSVLTQVLALLLWLTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
Humanized (22) Humanized nt (sense) Humanized nt (anti-sense)	, k.77/8×1	Q I Q I V Q S G S E I K K P G A S V K I S C K A S G Y T F T N T T G M N W V R Q A P G Q G T T T T O T T T T T T T T T T T T T T
Humanizad (aa) Humanizad nt (antaa) Humanizad nt (antaansa)	h77A3-1	G D E W M G W I N T K S G E P T Y A E B F K G R F V F S D D F S V S T A Y D Q I S S D C CON TOTAL AND CONTROL AND
Humanized (aa) Humanized nt (sense) Humanized nt (sent-sense)	h77A3-1	KAEDTAVYFCARWVPGT

h7743-2 HEAVY CHAIN SEQUENCES

		Signal Peptide
Humanized (aa) Humanized m (sense) Humanized m (and-temes)	h77A3 .2	M S V L T Q V L A L L L L W L T G A R C COA 7770 CAA 7770 COA 6770 COT COT COT COA 6770 COT COA 6770
Humanized (aa) Humanized nt (sense) Humanized nt (antisense)	h77A3.2	Q I Q L V Q S G A B V K K P G A S V K I S C K A S G Y T F T N Y COLO ANT CALO TOTO TOTO COLO TOTO COLO COTO TOTO COLO ANT CALO COLO COLO COLO COLO COLO COLO COLO
Humanized (aa) Humanized nt (sense) Humanized nt (annisense)	k71A 3 &	COLEWMGWIN THE KSGEPTYAEEFKGRFTROOTTH AND THE
Humanized (ag) Humanized nt (sense) Humanized nt (anti-sense)	h77A3.2	RSDDTAVYFCARMWVPGTACTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOT

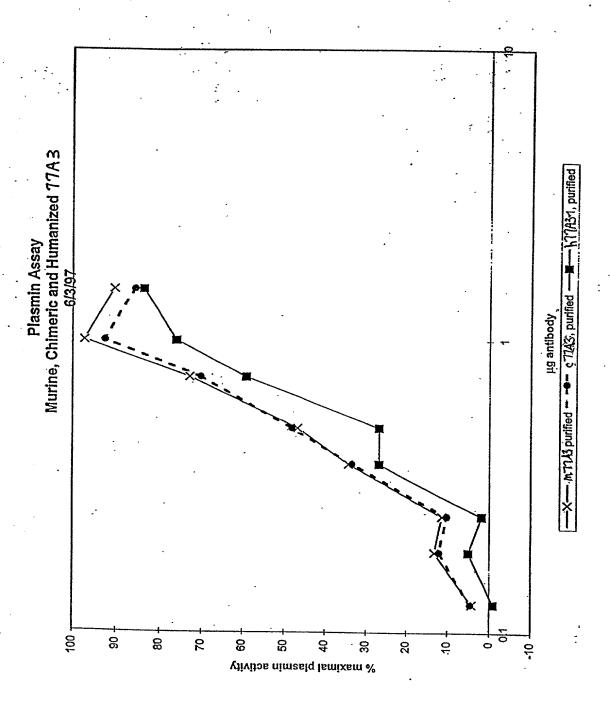


Figure 21

α2-antiplasmin antibody light chain sequences

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h77A3-1 and	h77A3-2	w	Y (ם ג	.K	Q	G #	: (S	P	Q.	LL	. v	Y	N A	ĸ	τ·l	_ `A	s	G١	/ P	8	R	F	S	Ġ	s (3 S	G	T	D I	F T	Ŀ	T
	m77A3 m49C9 m70B11	W W W	Y.C	3 0	K	Q	GH	(5	P	Q		V	YI	A P	. KI	TI	_ A	D	G١	V.P	S	R	F	S	G.	s (38	G	Ŧ.	Q	f s	L	R
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h77A3-1 and	h77A3-2	- 1	8	8 L	Q	P	E.I) F	G	S	НΥ	(C	Q.	HF	W	Τ:	T F	•					W	Ŧ	F	G (3 G	T	K	L	E. 1		K
•	m77A3 m49C9 m70B11	1	N.	sι	a	P.	EI	DF	G	S	ዘ ነ የ ነ	(0	Q	ΗJF	·W	Τ.	T F	•		·.			W	T	F	G (G (0 G (0	ÌŤ	K	L	Ē		K K
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Figure 2

Apple Company	α2-antip	lasmin ant	ibody hea	vy chain	sequences
			***	H1 Loop	
		1			1 .
h77A3-1 h77A3-2	SOVJOLOS	GSELKKPGAS GAEVKKPGAS	VKISCKAS VKISCKAS	YTFTNY YTFTNY	GMNWVRQAPGQ GMNWVRQAPGQ
m77A3 m49C9 m70B11	POLICIA	GPELKKPGET GPELKKPGET GPELKKPGET	VKIBCEASI	SY I FUNTI .	GMNWVKQAPGK GMNWVKQAPGK GMNWVKQAPGK
humanized consensus murine consensus 77A3/49C9 consensus all	QIQLVQS	GXEXKKPGAS GPELKKPGET GPELKKPGET GXEXKKPGXX	VKISCXAS	SYTETNY	GMNWVRQAPGQ GMNWVKQAPGK GMNWVKQAPGK GMNWVXQAPGX
			i.		
	· · · · · · · · · · · · · · · · · · ·	H2 Loop			
	1.	3	*		å Babc
h77A3-1 h77A3-2	G L EWMGW		TYAEEFKG Tyaeefkg	RFVF8LDTS RFTFTLDTS	SVSTAYLQ186L STSTAYLE1RSL
m77A3 m49C9 m70B11	G L KWMGW G L KWMGW G L KWMGV	VINT KSCEF	7 Y A E E E K (A)	RFVFSLET	SASTANLQIKNL BASTAHLQIKNF SASTAYLQINNL
humanized consensus murine consensus 77A3/49C9 consensus all	G L XWWGA G L KWWGA G L EMWGA	VINT KSCEF VINT XSCEF VINT KSCEF	TYAEEFKG	RFXFSLET:	SXSTAYLXIXSL SASTAXLQIXNX SASTAXLQIKNX SXSTAXLXIXXX
•	· L		H3 Loop	•	
	4	8	o a b c d o f a	6 6 6 4	1 1 0
h77A3-1 h77A3-2	KAEDTA' RSDDTA	VYFCARWVPG	T T	YAMDYWG YAMDYWG	QGTTVTVSS QGTTVTVSS
m77A3 m49C9 m70B11	RNEDTA	TYFCARWVPG TYFCARWVPG TYFCARWVPG	Ŧ	Y A M DÌYÎW G	QGTSVTVSS QGTSVTVSS QGTSVTVSS
humanized consensus murine consensus 77A3/49C9 consensus all	XNEDXA XNEDTA	VYFCARWYPG TYFCARWYPG TYFCARWYPG XYFCARWYPG	T	Y AMDYWG	QGTTVTVSS QGTSVTVSS QGTSVTVSS QGTXVTVSS